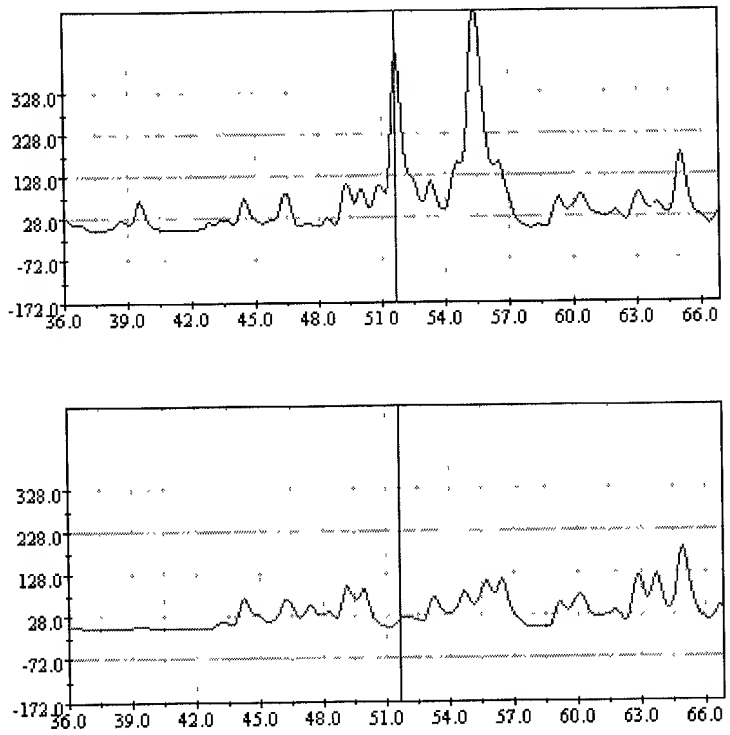
328.0
228.0
128.0
28.0
-72.0
-172.0
36.0 39.0 42.0 45.0 48.0 51.0 54.0 57.0 60.0 63.0 66.0
328.0
228.0
128.0
28.0
-72.0
-172.0
36.0 39.0 42.0 45.0 48.0 51.0 54.0 57.0 60.0 63.0 66.0

Figure 1

```
; GAP of: W0h051-7.Seq  check: 6926  from: 1  to: 52

seq of dicamba induced band w0c0 51.7

 to: Cjlpi81r.Seq  check: 2737  from: 1  to: 714


 Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Nwsgapdna.Cmp
 CompCheck: 8760

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      Length Weight:      3   Average Mismatch:  0.000

            Quality:    520             Length:    714
              Ratio: 10.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

        Match display thresholds for the alignment(s):
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                    : =   5
                    . =   1

 W0h051-7.Seq x Cjlpi81r.Seq..

                    .         .         .         .         .
       1 .........................gctagctgcgccgtgaccacgcacat 26
                                  ||||||||||||||||||||||||||
       1 CGATCGAAGTGGGTGTGTCAGCTAGCTAGCTGCGCCGTGACCACGCACAT 50
                    .         .         .         .         .
      27 gaccgcagtgcgcgcggggctgatca.......................... 52
         ||||||||||||||||||||||||||
      51 GACCGCAGTGCGCGCGGGGCTGATCAAGGGAAAGTGATCGGATGGAGCTG 100
```

Figure 2

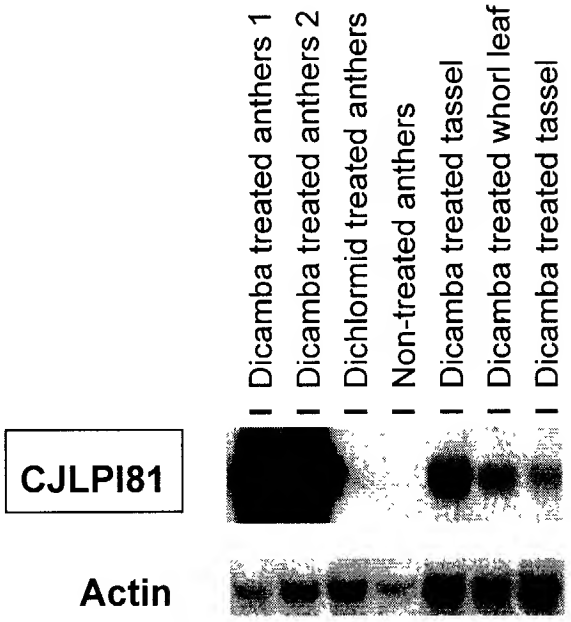

Figure 3

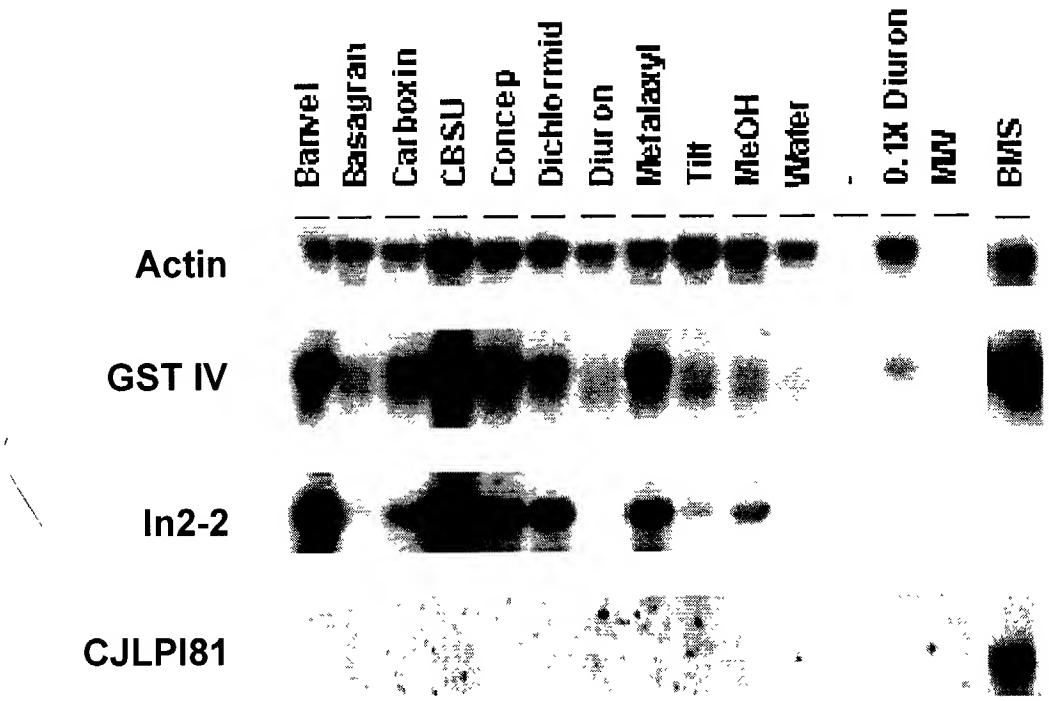

Figure 4

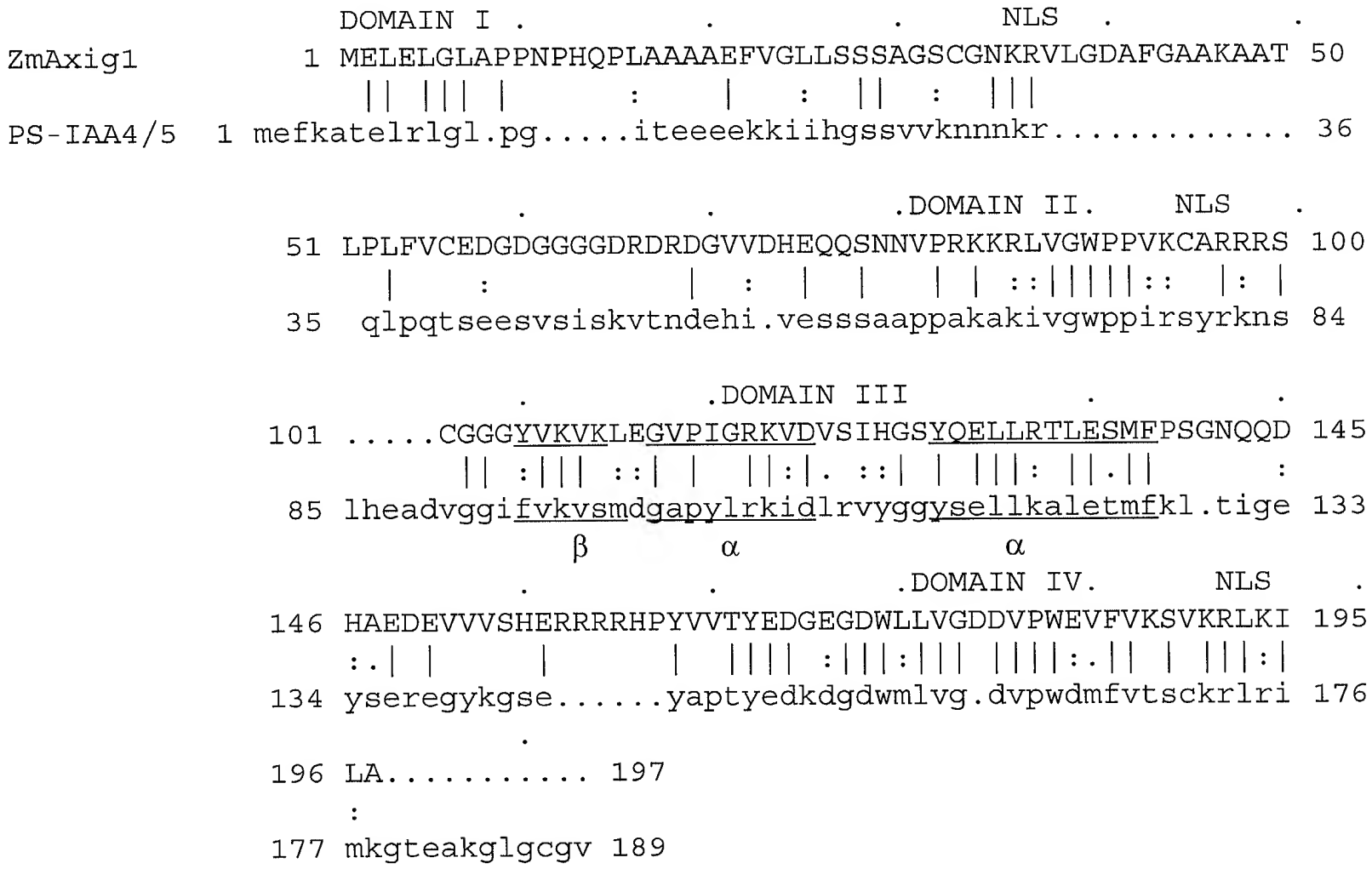
DOMAIN I
NLS
ZmAxig1 1 MELELGLAPPNPHQPLAAAAEFVGLLSSSAGSCGNKRVLGDAFGAAKAAT 50
PS-IAA4/5 1 mefkatelrlgl.pg.....iteeeekkiihgssvvknnnkr..... 36
DOMAIN II.
NLS
51 LPLFVCEDGDGGGGDRDRDGVVDHEQQSNNVPRKKRLVGWPPVKCARRRS 100
35 qlpqtseesvsiskvtndehi.vesssaappakakivgwppirsyrkns 84
DOMAIN III
101 .....CGGGYVKVKLEGVPIGRKVDVSIHGSYQELLRTLESMFPSGNQQD 145
85 lheadvggifvkvsmdgapylrkidlrvyggysellkaletmfkl.tige 133
β
α
α
DOMAIN IV.
NLS
146 HAEDEVVVSHERRRRHPYVVTYEDGEGDWLLVGDDVPWEVFVKSVKRLKI 195
134 yseregykgse.....yaptyedkdgdwmlvg.dvpwdmfvtsckrlri 176
196 LA..... 197
177 mkgteakglgcgv 189

Figure 5

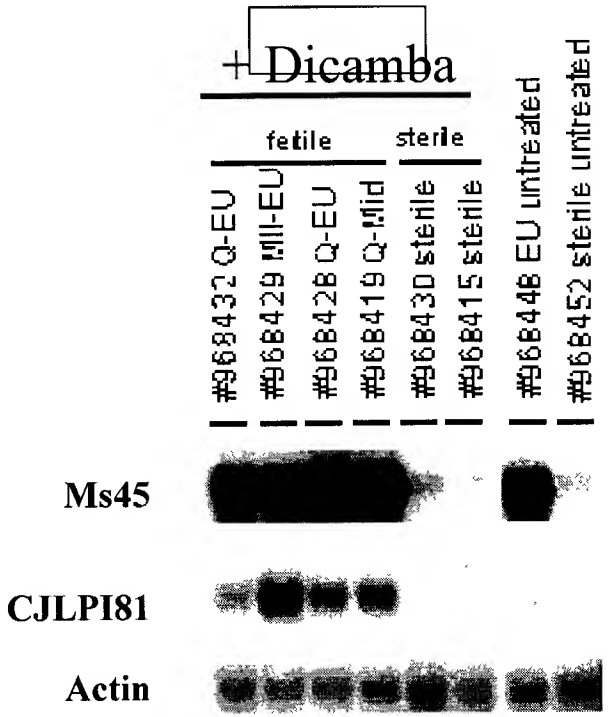

Figure 6

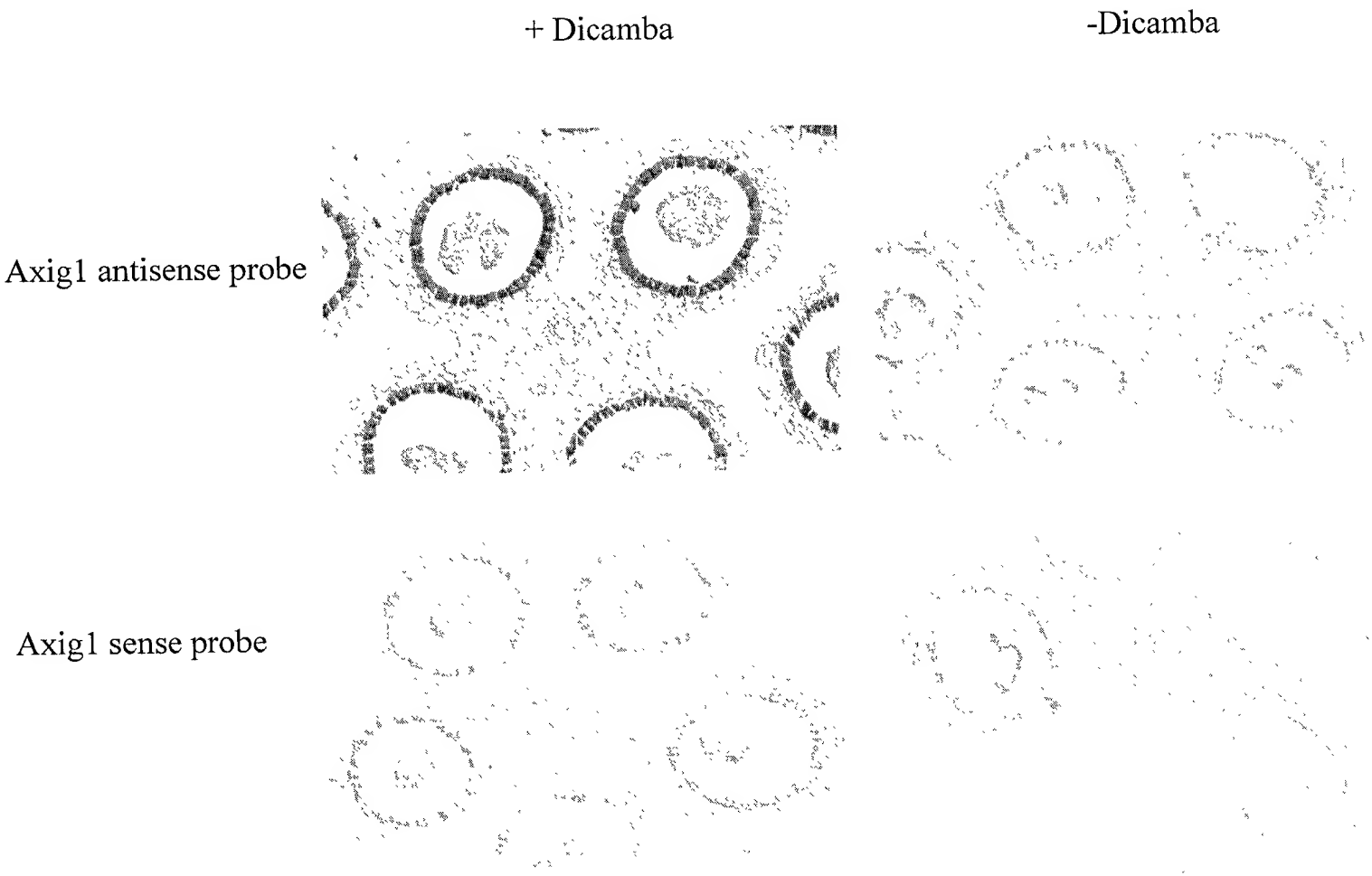

Figure 7

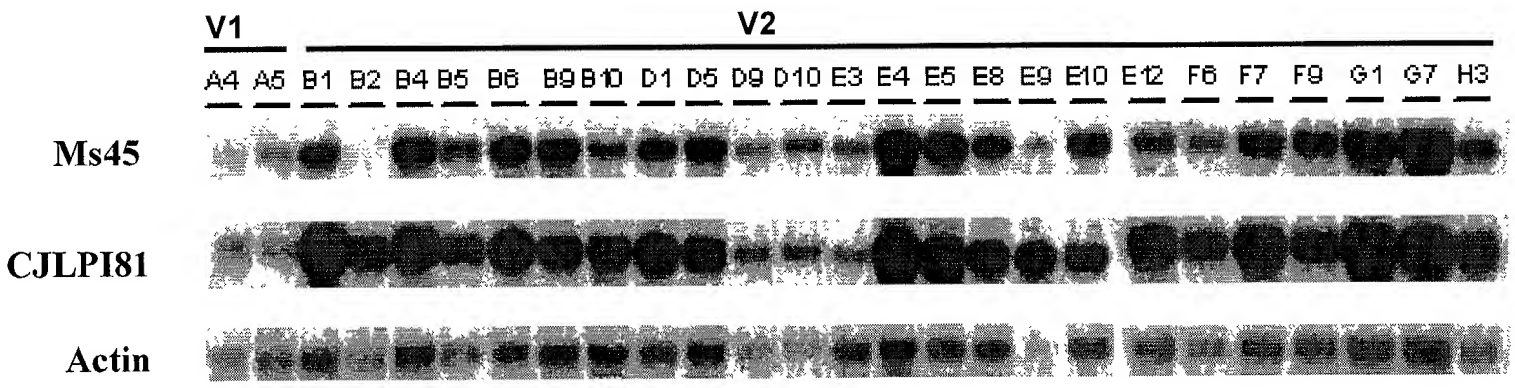
V1
V2
A4 A5 B1 B2 B4 B5 B6 B9 B10 D1 D5 D9 D10 E3 E4 E5 E8 E9 E10 E12 F6 F7 F9 G1 G7 H3
Ms45
CJLPI81
Actin

Figure 8

Figure 9

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    to: Axig1complete.Con  check: 928  from: 1  to: 3123

 Symbol comparison table:
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 CompCheck: 8760

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      Length Weight:       3   Average Mismatch:  0.000

            Quality:  10871              Length:   3123
              Ratio:  8.955                Gaps:      3
 Percent Similarity: 100.000   Percent Identity: 100.000

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                    . =    1

 Czaal47.Seq x Axig1complete.Con May 11, 2000 12:05  ..

                                              .
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   1 ......................................GCAGGAACTTAT 12
                                           ||||||||||||
1101 CGCGTCACTCACGGGTAGCTCATGGTCGAGCGTAGCATGCAGGAACTTAT 1150
             .         .         .         .         .
  13 TTGCCGTGCGCTCCCAGGTCTCCGCTCGCGTGCCTTCCAGTCTGTCTCAC 62
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1151 TTGCCGTGCGCTCCCAGGTCTCCGCTCGCGTGCCTTCCAGTCTGTCTCAC 1200
             .         .         .         .         .
  63 ACTAGCTGCTGTGGGACGATCGAAGTGGGTGTGTCAGCTAGCTAGCTGCG 112
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1201 ACTAGCTGCTGTGGGACGATCGAAGTGGGTGTGTCAGCTAGCTAGCTGCG 1250
             .         .         .         .         .
 113 CCGTGACCACGCACATGACCGCAGTGCGCGCGGGGCTGATCAAGGGAAAG 162
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1251 CCGTGACCACGCACATGACCGCAGTGCGCGCGGGGCTGATCAAGGGAAAG 1300
             .         .         .         .         .
 163 TGATCGGATGGAGCTGGAGCTCGGGCTCGCGCCGCCGAACCCGCATCAGC 212
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1301 TGATCGGATGGAGCTGGAGCTCGGGCTCGCGCCGCCGAACCCGCATCAGC 1350
             .         .         .         .         .
 213 CGCTGGCTGCCGCCGCCGAGTTCGTCGGTCTCCTCAGCAGCTCGGCTGGC 262
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1351 CGCTGGCTGCCGCCGCCGAGTTCGTCGGTCTCCTCAGCAGCTCGGCTGGC 1400
             .         .         .         .         .
 263 TCGTGCGGGAACAAGAGGGTTCTCGGCGACGCGTTCGGGGCCGCCAAGGC 312
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1401 TCGTGCGGGAACAAGAGGGTTCTCGGCGACGCGTTCGGGGCCGCCAAGGC 1450
             .         .         .         .         .
 313 GGCCACGCTTCCGCTCTTCGTCTGCGAGGATGGCGACGGAGGCGGCGGCG 362
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1451 GGCCACGCTTCCGCTCTTCGTCTGCGAGGATGGCGACGGAGGCGGCGGCG 1500
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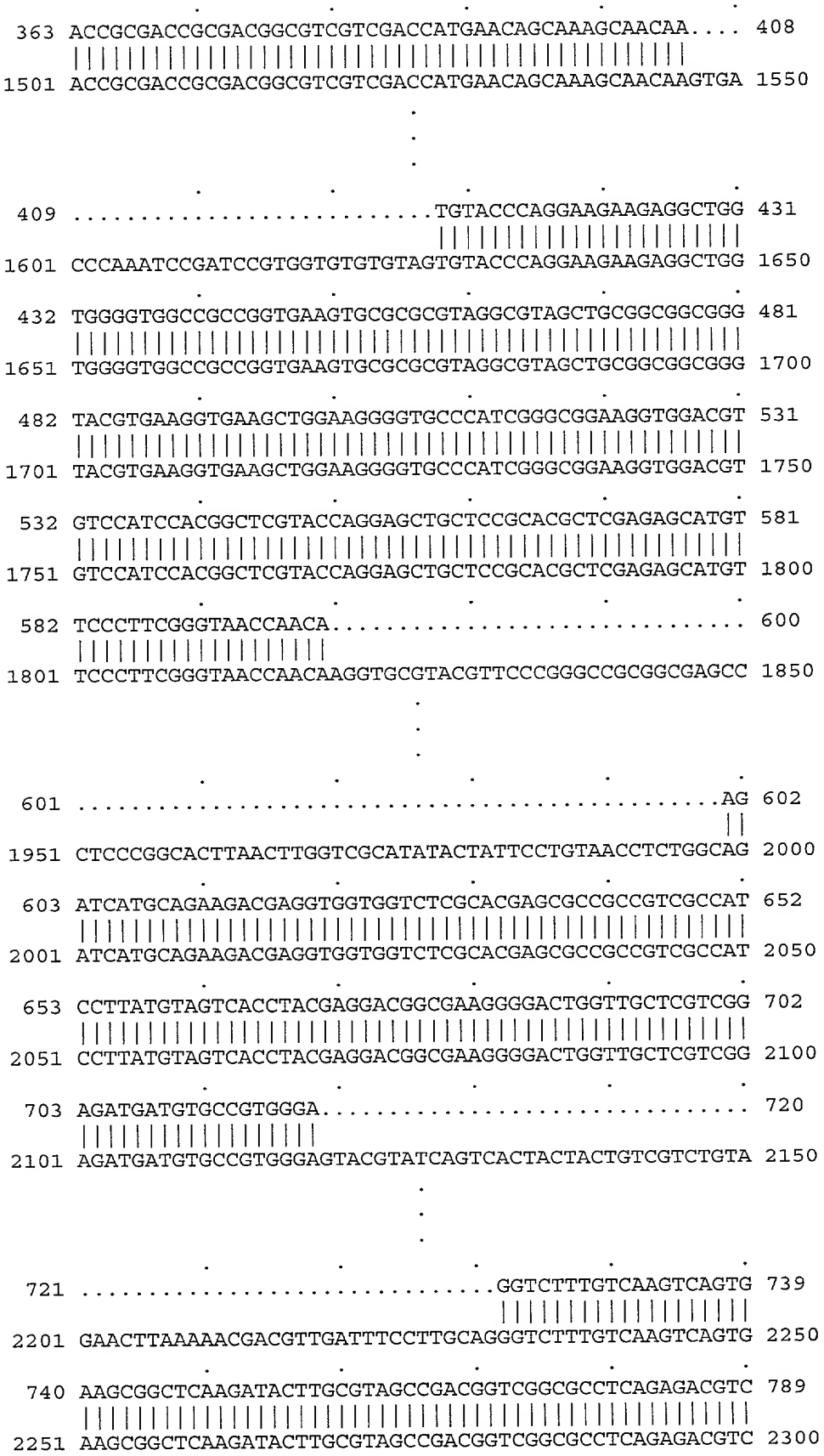
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1501 ACCGCGACCGCGACGGCGTCGTCGACCATGAACAGCAAAGCAACAAGTGA 1550
409 .....TGTACCCAGGAAGAAGAGGCTGG 431
1601 CCCAAATCCGATCCGTGGTGTGTGTAGTGTACCCAGGAAGAAGAGGCTGG 1650
432 TGGGGTGGCCGCCGGTGAAGTGCGCGCGTAGGCGTAGCTGCGGCGGCGGG 481
1651 TGGGGTGGCCGCCGGTGAAGTGCGCGCGTAGGCGTAGCTGCGGCGGCGGG 1700
482 TACGTGAAGGTGAAGCTGGAAGGGGTGCCCATCGGGCGGAAGGTGGACGT 531
1701 TACGTGAAGGTGAAGCTGGAAGGGGTGCCCATCGGGCGGAAGGTGGACGT 1750
532 GTCCATCCACGGCTCGTACCAGGAGCTGCTCCGCACGCTCGAGAGCATGT 581
1751 GTCCATCCACGGCTCGTACCAGGAGCTGCTCCGCACGCTCGAGAGCATGT 1800
582 TCCCTTCGGGTAACCAACA..... 600
1801 TCCCTTCGGGTAACCAACAAGGTGCGTACGTTCCCGGGCCGCGGCGAGCC 1850
601 .....AG 602
1951 CTCCCGGCACTTAACTTGGTCGCATATACTATTCCTGTAACCTCTGGCAG 2000
603 ATCATGCAGAAGACGAGGTGGTGGTCTCGCACGAGCGCCGCCGTCGCCAT 652
2001 ATCATGCAGAAGACGAGGTGGTGGTCTCGCACGAGCGCCGCCGTCGCCAT 2050
653 CCTTATGTAGTCACCTACGAGGACGGCGAAGGGGACTGGTTGCTCGTCGG 702
2051 CCTTATGTAGTCACCTACGAGGACGGCGAAGGGGACTGGTTGCTCGTCGG 2100
703 AGATGATGTGCCGTGGGA..... 720
2101 AGATGATGTGCCGTGGGAGTACGTATCAGTCACTACTACTGTCGTCTGTA 2150
721 .....GGTCTTTGTCAAGTCAGTG 739
2201 GAACTTAAAAACGACGTTGATTTCCTTGCAGGGTCTTTGTCAAGTCAGTG 2250
740 AAGCGGCTCAAGATACTTGCGTAGCCGACGGTCGGCGCCTCAGAGACGTC 789
2251 AAGCGGCTCAAGATACTTGCGTAGCCGACGGTCGGCGCCTCAGAGACGTC 2300

```
       .         .         .         .         .
 790 GTGTGGTCCGTCTCACCAGGATCGGAGCAGTGTAGTACTCCTGGGCGTCA 839
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2301 GTGTGGTCCGTCTCACCAGGATCGGAGCAGTGTAGTACTCCTGGGCGTCA 2350
       .         .         .         .         .
 840 TCTGCGTAATAACGTTGTTTCTGTCCTGTGTGCCCGTAGCAGTACGTACT 889
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2351 TCTGCGTAATAACGTTGTTTCTGTCCTGTGTGCCCGTAGCAGTACGTACT 2400
       .         .         .         .         .
 890 GTCCTATAGTAAGCTAGCTTTATGGGGTGCTTCAGCTTTCAGAGCATGAC 939
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2401 GTCCTATAGTAAGCTAGCTTTATGGGGTGCTTCAGCTTTCAGAGCATGAC 2450
       .         .         .         .         .
 940 GAAAGCACTGATTAGCTGCTGTCATCACATTTGGTTCGTCTTTGTGTCGT 989
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2451 GAAAGCACTGATTAGCTGCTGTCATCACATTTGGTTCGTCTTTGTGTCGT 2500
       .         .         .         .         .
 990 ACGGTATCGCTGGCGTCAGTGTCGCGGCAGCCTAGGTGATCTAAGCATAC 1039
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2501 ACGGTATCGCTGGCGTCAGTGTCGCGGCAGCCTAGGTGATCTAAGCATAC 2550
       .         .         .         .         .
1040 TTACTATCTCAAGTTACTTTTGGTTTCCTGAGCTTGCATGGTAATTCATA 1089
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2551 TTACTATCTCAAGTTACTTTTGGTTTCCTGAGCTTGCATGGTAATTCATA 2600
       .         .         .         .         .
1090 TACCGTATACGTGTGTGACTCAGGGGCGAAGCTGCCTTAAGGCACAGGGG 1139
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2601 TACCGTATACGTGTGTGACTCAGGGGCGAAGCTGCCTTAAGGCACAGGGG 2650
       .         .         .         .         .
1140 TCACCGGACCCGATGGAATTTATCAAATCCAGTGTAAAATACTATTTAAC 1189
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2651 TCACCGGACCCGATGGAATTTATCAAATCCAGTGTAAAATACTATTTAAC 2700
       .         .         .         .         .
1190 ACTGTTCATCAATATATTTGATTTC......................... 1214
     |||||||||||||||||||||||||
2701 ACTGTTCATCAATATATTTGATTTCAATAATTCATGGAGCTGACCTTGTG 2750
                              .
                              .
                              .
```

Sequence Name		SEQ ID NO:	ATCC Deposit
Pioneer clone CZAAL47		1	PTA-2426
ZmAxig1 polypeptide		2	
Native ZmAxig1 promoter region		3	
Modified ZmAxig1 promoter region		4	PTA-2427
A632 full-length ZmAxig1, including SEQ ID No. 3		5	PTA-2426 PTA-2427
Primer 1, used for isolation of 5'flanking region		6	
Primer 2, used for isolation of 5'flanking region		7	
Primer 3, used for isolation of region spanning start codon		8	
Primer 4, used for isolation of region spanning start codon		9	
Primer 5, used for isolation of 5' region		10	
Oligonucleotide designed to remove clones having a poly-A tail but no cDNA		11	
Pioneer clone Cjlpi81		12	
CuraGen fragment w0h051.7		13	
Primer 6, used to isolate the coding sequence and 3' region		14	
Primer 7, used to isolate the coding sequence and 3' region		15	
Modified ZmAxig1 promoter region with single-base deletion		16	PTA-2427
LEC1 transcriptional activator element		17	
LEC1 polynucleotides		18-20	
LEC1 polypeptide consensus sequence		21	

Figure 10. Representative polynucleotides and polypeptides of the present invention.

Experiment	Control	Ubi:LEC1	Axig1:LEC1
#1 3938.37	15%	63%	44%
#2 3938.79	4%	17%	20%
#3 3938.78	16%	17%	38%
#4 3938.34	2%	14%	13%

Figure 11. Transformation frequencies by LEC1 with two different promoters. Transformation frequencies were based on the percentage of plated embryos with one or more GFP positive/Bialaphos resistant colonies. All embryos were shot with Ubi:moPAT~GFP (a construct conferring Bialaphos resistance and GFP fluorescence) along with a LEC1 construct or a control DNA.